

**Comparison of Expected and Actual Progeny Growth Differences in
Crossbred Calves**

by

Garry Sonn Mahrt

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APPROVED:

D. R. Notter, Chairman

A. L. Eller

R. E. Pearson

W. E. Vinson

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(ABSTRACT)

The growth performance of Angus-Polled Hereford F₁ calves was compared to the expected progeny differences (EPD) estimated by the American Polled Hereford Association to evaluate the usefulness of EPD estimates for improving commercial beef production.

Polled Hereford sires were selected from the high accuracy sires listed in the American Polled Hereford Association's sire summary. Four types of sires were used: 1) Sires with high yearling weight and high maternal EPD's; 2) Sires with high yearling weight and low maternal EPD's; 3) Sires with low yearling weight and high maternal EPD's; and 4) Sires with low yearling weight and low maternal EPD's.

The resulting progeny were weighed at birth, approximately 135 d, weaning and approximately 1 yr. Hip heights were also measured at weaning. Linear regressions of progeny performance on EPD indicated that birth and yearling weights were accurately predicted by their respective EPD estimates. Weight and height at weaning were not accurately predicted by weaning weight EPD. Partial regressions of progeny performance on yearling weight and maternal EPD's were also calculated. Regression of progeny performance on yearling weight EPD resulted in

.16 ± .09 kg/kg for 135-d weight, .28 ± .09 kg/kg for weaning weight, .073 ± .020 cm/kg for weaning hip height and .93 ± .19 kg/kg for yearling weight. Comparable regression values for maternal EPD were .44 ± .18 kg/kg, .31 ± .17 kg/kg, .100 ± .040 cm/kg and .22 ± .36 kg/kg for 135-d, weaning weight, weaning hip height and yearling weight, respectively. These results indicate that maternal EPD values predicted some differences in preweaning growth that were not predicted by yearling weight EPD.

The progeny performance data was also used to calculate independent EPD estimates for birthweight, weaning weight, and yearling weight. Correlations between these EPD estimates and those made by the American Polled Hereford Association were .49 for birthweight, .26 for weaning weight and .66 for yearling weight. The low correlation between weaning weight EPD estimates was significantly below expectation and indicates that the American Polled Hereford Association estimates were inadequate for predicting preweaning growth differences in these cross-bred calves.

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INTRODUCTION

The use of national sire evaluations (NSE) has been credited for increased performance in purebred cattle. Positive genetic trends for live weight at weaning and at one year of age were reported for registered Angus, Hereford and Simmental cattle in the United States (Benyshek, 1986 ; Elzo et al., 1987). Since registered purebred cattle represent the genetic nucleus that supplies germ plasm to the commercial beef industry, the performance gains reported for purebred cattle should also be occurring in commercial cattle herds. Commercial beef herds tend to be less intensively managed than purebred herds and utilize varying degrees of crossbreeding. These differences between the two segments of the beef industry may partially invalidate the premise that genetic gains from the use of NSE are being passed on to the commercial cattle industry from purebred herds.

This thesis will examine the utility of the NSE and its published estimates of sire genetic values (i.e., expected progeny differences; EPD) as tools for enhancing commercial beef production. Results from an experiment comparing the actual performance of crossbred progeny from unregistered commercial Angus cows to sire EPD values reported by the American Polled Hereford Association (APHA) are presented to evaluate one NSE program as a tool for commercial cattle breeders.

LITERATURE REVIEW

SIRE SUMMARIES

The relatively small effective herd size and long generation interval in beef cattle limits the selection intensity in cattle breeding relative to other livestock species such as poultry and swine. Three possible methods of increasing the effective population size, and therefore the selection intensity, in private herds were outlined by Parnell et al. (1986):

1) Establishment of genetic links between herds through the use of artificial insemination (AI) and reference sires. This method facilitates comparisons of many sires across herds and is the fundamental principal of NSE.

2) Use of central test stations to evaluate bulls or their progeny. This method also allows for multi-herd comparisons of sires.

3) Nucleus breeding schemes in which member farms contribute superior animals to a common herd that is more intensively selected and managed for the production of herd sires.

The first two methods have been widely used in the U.S. Central test stations have been useful, but generally their evaluations only provide information on postweaning gains. Postweaning growth is only one component of the cattle production system and its relative importance in the overall production of beef is debatable. In contrast the use of reference sires to progeny test sires within and across herds allows many

traits to be evaluated. Currently most beef breed organizations recommend progeny testing of sires for birth weight (BWT), weaning or 205-d weight (WWT), yearling or 365-d weight (YWT), and maternal ability (MAT) of a sire's daughters, which is measured by the WWT of the daughters' first calves. Other traits evaluated include carcass quality traits and calving ease (BIF, 1986). The results of these progeny tests are evaluated using NSE methods.

NSE systems for beef cattle have been developed by adapting and modifying methodology that was originally developed for evaluation of dairy sires. Henderson (1973) recognized the need for evaluating dairy sires using information from many herds. All of the current theory and application of NSE stems directly from Henderson's work. The first methods of NSE that were developed compared sires used in designed breeding programs which stressed random matings between sires and the available dams within each herd or contemporary group (CG). Analysis required a model that included fixed environmental effects and random genetic effects of sires; hence the designation of mixed model solutions (MMS) to describe the results of these evaluations. Berger (1983) has described the basic sire model for beef sire evaluation as:

Equation 1.

$$y_{ijk} = \mu + CG_i + S_j + \varepsilon_{ijk}$$

where:

μ = population mean

y_{ijk} = record of k^{th} progeny from
the j^{th} sire in the
 i^{th} contemporary group

CG_i = fixed effect of i^{th} contempo-
rary group

S_j = random effect of j^{th} sire

ε_{ijk} = residual

Contemporary groups are used to group progeny reared under similar environmental or fixed effects (e.g., year, herd, sex, etc.). Equation 1 can be written in matrix notation, which is generally more appropriate for MMS procedures, as:

Equation 2.

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\mu} + \boldsymbol{\varepsilon}$$

where:

\mathbf{y} = vector of progeny records

\mathbf{X} = incidence matrix of fixed effects

$\boldsymbol{\beta}$ = vector of fixed effects

\mathbf{Z} = incidence matrix of random sire effects

$\boldsymbol{\mu}$ = vector of random sire effects

$\boldsymbol{\varepsilon}$ = vector of random residual effects

The preceding equations will generate solutions for the sire and fixed effects, but these solutions do not consider sires as random effects, nor accurately account for unequal progeny numbers. Even in designed breeding experiments, unequal subclass numbers are the rule rather than the exception because of variable conception and birth rates. Henderson (1973) modified the matrices to account for unbalanced sampling of sire effects as:

Equation 3.

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \beta \\ \mu \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

where:

$$VAR \begin{bmatrix} \mu \\ \varepsilon \end{bmatrix} = \begin{bmatrix} G & \emptyset \\ \emptyset & R \end{bmatrix}$$

and where:

β = estimate of fixed effects

μ = estimate of random sire effects

The residual variance matrix (R) usually consists of an identity matrix (I) multiplied by the residual variance for the model. The matrix of sire variance components (G) can include the covariance between sires if relationships between sires are known. The addition of the variance matrices (R and G) to the matrix equations has the greatest effect on

sires with relatively fewer offspring. The solutions for those sires with limited information are regressed back towards the mean so that they can be directly compared to expected progeny differences (EPD's) generated for sires with more progeny information. This gives the MMS similar properties as selection indexes but expands their usefulness beyond selection within CG's. These MMS are considered to be best linear unbiased predictors (BLUP) of the true breeding values of the sires. Properties of BLUP estimates include: 1) minimum error variance for an unbiased predictor; 2) maximum correlation between true value and estimates; 3) if both the data set and true values have multivariate normal distributions, then estimates maximize the probability of the correct pairwise ranking of sires; and 4) the estimates are unbiased (Van Vleck, 1983). Another important feature of Henderson's MMS analysis is that only the second moment of the distribution is needed. Direct estimates of the magnitude and direction of fixed effects are not needed to properly evaluate sires.

Limiting sire proofs to designed progeny tests resulted in evaluation of fewer sires and use of less information than would be possible if all the available field data could be used. The Beef Improvement Federation (BIF) published its first guidelines for performance recording in 1968 (BIF, 1986). Promotion and development of performance recording and objective methods of selection continue to be the goals of BIF. The introduction of European germ plasm to North America in the early 1970's helped to advance progeny testing towards the first published NSE (Parnell et al., 1986). Many of the newly formed breed organizations

required that all registered cattle have performance records on production traits (e.g., WWT, YWT). Initial importations of the European germ plasm were limited to semen from a few sires. The wide use of a small group of sires through AI expanded the reference sire concept into a workable method for utilizing all field records of a breed to conduct a NSE. A reference sire is defined as a sire that is used across many herds so that EPD's for sires with progeny in only one herd can be compared against a common genetic benchmark. In this way, MMS for sire and fixed effects can be made across all herds in the population. With widespread use of AI, many sires can qualify as reference sires and the use of designated reference sires in designed programs becomes unnecessary. In 1971 BIF published guidelines for beef cattle NSE (Berger, 1983) and in 1972 the American Simmental Association published the first NSE (Warwick, 1980). The first sire summary utilized progeny data from both designed tests and field data with reference sires to connect the data.

As more field data became incorporated into NSE, the larger data sets required improved computing techniques and hardware. Henderson (1974) outlined some of the important considerations to be made when utilizing field data. Sire EPD estimation improves as the genetic connections between herds increases through the use of reference sires. Even though the use of reference sires has been emphasized from the beginning of NSE development, a large number of progeny records must still be deleted from NSE computations because some CG's contained progeny from only one sire (Gibb and Middleton, 1986). Henderson also

emphasized the importance of including all major sources of variation and bias in the sire model whenever computationally possible.

Genetic trend has been identified as a major source of bias, since progeny records made in earlier generations are not directly comparable to those made today. The average genetic performance should be higher now than in previous generations. This complication led to the addition of the sire birth year effect in the basic sire model (Berger, 1983):

Equation 4.

$$y = X\beta + ZQ\gamma + Z\mu + \varepsilon$$

where:

$$VAR \begin{bmatrix} \mu \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A/\alpha & 0 \\ 0 & I \end{bmatrix} \sigma_{\varepsilon}^2$$

$$\alpha = \sigma_{\varepsilon}^2 / \sigma_{\mu}^2$$

A = matrix of relationships between sires

$$A/\alpha = G$$

Q = incidence matrix relating sire birth year effects to sires

γ = vector of fixed sire birth year effects

The sire variance-covariance matrix (G) has been expressed as the product of the sire relationship matrix (A) and variance component estimates to emphasize the importance of the sire relationship matrix. The sire relationship matrix allows information from all related sires to contribute to a sire's proof. If sires are assumed to be unrelated and an

identity matrix (I) is substituted for A, then only information from a sire's progeny will contribute to his proof.

The sire birth year effect is the average genetic value of the population when most of a sire's progeny were evaluated. At a point in time the mean of the population is fixed, so the sire birth year is a fixed effect. The expected progeny difference (EPD) of a sire is then expressed as the sum of the sire effect and the appropriate sire birth year group effect.

Use of field data increased the size of available data sets to the limits of computer capabilities. To save computer time, the CG effects are absorbed into the sire equations. The result of such absorbtion is that CG effects are accounted for in NSE but no attempt is made to solve them directly. The folowing is the matrix representation of equation 4 with absorbed CG effects (Berger, 1983).

Equation 5.

$$\begin{bmatrix} Q'Z'MZQ & Q'Z'MZ \\ Z'MXQ & Z'MZ + A^{-1} \end{bmatrix} \begin{bmatrix} \gamma \\ \mu \end{bmatrix} = \begin{bmatrix} Q'Z'My \\ Z'My \end{bmatrix}$$

where:

$$M = I - X(X'X)^{-1}X'$$

γ = estimate of sire birth year fixed effects

Absorption of CG effects modifies the basic matrix equations (3) so that progeny in the same CG are contrasted against each other to

estimate the contribution of the sire. The sum of all sire estimates across all CG's is then used to derive sire EPD estimates.

The sire birth year effects must be constrained so that the resulting matrix is nonsingular and therefore solvable. Two methods of constraining the sire birth year effects are recommended by BIF (1986). One sire birth year, usually corresponding to the oldest sires, can be set at a value of zero. This results in a fixed base and all NSE's are comparable regardless of the year in which they were conducted. With a fixed base, a sire's EPD changes from year to year only as the information on his progeny changes. A drawback with fixed genetic bases is that the average reported EPD will continue to rise with the genetic trend of the population. This does not effect the general BLUP properties of a sire's EPD , but does cause herd owners to expect greater annual improvements from young bulls simply because their EPD's are higher then those of bulls used in earlier generations. New sires will have a greater impact only if the herds in which they are used have not improved with the genetic trend of the population. An alternative to a fixed base is a floating base that constrains the sum of all sire birth year effects to equal zero. When a floating base is used the resulting EPD's are unique for each evaluation since the value of a sire's birth year group varies with each evaluation. This constraint should not, however, effect the rankings of sires.

Another method of eliminating genetic trend bias in NSE is to use pedigree information on the sires (BIF, 1986). By using a relationship matrix that includes grandsires and earlier generations, any inflation of

the EPD of older sires will also increase the EPD of their descendants. This method became advantageous after Henderson (1975) demonstrated the ease with which the inverse of the full sire relationship matrix A^{-1} could be calculated when the sires' full pedigrees are used. This method proved to be computationally easier than calculating A^{-1} for only the relationships between sires and grandsires listed in the NSE. BIF (1986) also suggests a sire model that combines use of sire birth year groups and a partial relationship matrix that only includes sires and maternal grand sires. Such a model is recommended for large data sets, especially when pedigree information is incomplete (Berger, 1983).

Field data has another disadvantage relative to designed progeny data. Random mating is generally not practised by private herd owners. Assortative mating can be particularly a problem with sires that already have published NSE results. Industry wide knowledge of a sire's genetic worth can lead to bias if many herd owners use similar breeding strategies. Elimination of bias due to conscious selection of sire-dam mating pairs was the next step in NSE development. A random dam effect can be added to the sire model (BIF, 1986) to account for selection of sire-dam mating pairs:

Equation 6.

$$y = X\beta + Z_1Q\gamma + Z_1\mu_1 + Z_2\mu_2 + \varepsilon$$

where:

Z_1 = incidence matrix of random sire effects

μ_1 = vector of random sire effects

Z_2 = incidence matrix of random dam effects

μ_2 = vector of random dam effects

The number of equations that must be solved to estimate all effects in this model usually requires that most fixed effects and the random dam effects be absorbed before sire and sire birth year effects are estimated. Generally the dam and CG are first absorbed into herd effects and herd effects are subsequently absorbed into the sire equations. This procedure greatly reduces the number of equations that must be solved. Since only animals with progeny in several CG's (i.e., sires) are evaluated, dams and potential herd replacements must be selected using pedigree and within-herd information.

Quaas and Pollak (1980) proposed an animal model for within-herd selection that makes EPD estimates of both parents and progeny directly comparable. Progeny EPD's are calculated as the sum of half the parental EPD's and a regressed portion of the individuals' own record expressed as a deviation from expectation. Thus:

Equation 7.

$$EPD_i = \beta(y_i - EPD_s - EPD_d) + \frac{1}{2}EPD_s + \frac{1}{2}EPD_d$$

where:

EPD_i = breeding value of i^{th} nonparent

β = regression of genotype on phenotype

y_i = i^{th} individual's own record

EPD_s = EPD of sire

EPD_d = EPD of dam

The matrix notation for equation 7 was later described by Pollak and Quaas (1983) as:

Equation 8.

$$\begin{bmatrix} X'X & \emptyset & X' \\ \emptyset & A_{11}\alpha & A_{12}\alpha \\ X & A'_{12}\alpha & I + A_{22}\alpha \end{bmatrix} \begin{bmatrix} \beta \\ \mu_1 \\ \mu_2 \end{bmatrix} = \begin{bmatrix} X'y \\ \emptyset \\ y \end{bmatrix}$$

where:

A_{11} = relationship matrix of parents

A_{12} = incidence matrix of relationships between parents and non-parents

A_{22} = relationship matrix of non-parents

μ_1 = breeding value estimate of parents

μ_2 = breeding value estimate of non-parents

The above analysis requires that an equation be solved for every progeny record used. Such a large number of equations limits this process to within herd or subpopulation analysis. The animal model improves the selection process for young herd replacements. Unfortunately, the selection of yearling sires will be based on within herd information unless the animal model includes NSE data or involves several herds. The need to properly combine within-herd and NSE analysis procedures requires increased computer capabilities and computational simplifications of the animal model so that all individuals in all herds can be directly compared.

The reduced animal model (RAM) solves for the BV of all animals in the population that are parents and then uses these values to backsolve for nonparents using the principals set forth in the animal model (Pollak and Quaas, 1983). Advances in computer technology make it possible for breed organizations with moderately sized data sets to solve directly for dam and sire EPD's using RAM. For the larger data sets, absorption and back solution of both progeny and dam effects may be required (Wilson et al., 1985). The dam and progeny EPD values generated by this latter method are still directly comparable to those of proven sires, but their prediction error variances are larger than for EPD's generated by RAM. Increases in prediction error variances can be justified if the savings in computer time is substantial. The RAM and equivalent methodology moves purebred breeding beyond NSE to national animal evaluation (Benyshek, 1986).

Beef cattle selection usually is for a combination of growth, maternal and reproductive traits. Sequential selection often occurs as breeders select first for calves with acceptable BWT and then cull again at weaning and as yearlings to eliminate poor-growing individuals. Maternal performance is measured as the WWT of calves raised by a dam or daughters of a sire. Most currently published NSE's report sire EPD's for BWT, WWT, YWT and MAT traits in pounds of expected differences. After weaning, the effects of sequential selection become large and can bias the NSE since the records are no longer from the general population, but rather from a selected group of individuals. Yearling weights are particularly sensitive to this bias since WWT is a large component of YWT. Culling of low gaining individuals at weaning will make YWT EPD differences between sires less apparent. Postweaning gain can be measured instead of YWT to eliminate some of the bias from culling at weaning (Quaas and Pollak, 1980). With this procedure, EPD values are calculated for WWT and postweaning gain. A sire's EPD for YWT is then the sum of the WWT and postweaning gain EPD's. The poor gaining calves will still contribute to the YWT EPD of the sire and less information on gain to 365-d is lost when calves are culled at weaning.

Multiple trait analysis can also help to eliminate bias in NSE. This type of analysis combines all the information on correlated traits and uses estimated variances and covariances of the traits to solve for a sire's EPD. The multiple trait procedures garner more information from the available data, thereby increasing accuracy and especially adding information to EPD values for sex limited and lowly heritable traits (Henderson

and Quaas, 1986). Multiple trait analysis requires that the RAM matrix equations be expanded to include all related traits. The matrix of animal effects is then augmented by the covariance between traits and EPD's for all traits are obtained simultaneously. This procedure greatly increases the number of equations to be solved.

The accuracy of estimates of MAT effects can also be improved by multiple trait analysis. Since maternal effects are measured as WWT of a calf, many effects can be confounded. The direct inheritance of growth genes from the sire and dam as well as the maternal environment provided by the dam contribute to each WWT record. Only a multiple trait analysis can accurately define these three different factors by solving for all of them simultaneously using all available information and known biological relationships (Quaas and Pollak, 1980). Of course all the benefits of multiple trait analysis come at the expense of increased computer time and cost. Alternative methods are cheaper but rely on assumptions of randomness that are not true for most data sets.

Another statistic furnished along with each EPD in a sire summary is the accuracy (ACC) figure. Accuracy represents the correlation between an EPD and the true genetic value of a parent (Henderson, 1973).

Equation 9.

$$ACC = 1 - (\text{Prediction Error VAR}) / (\text{Sire VAR})$$

where:

ACC = accuracy of EPD estimate

VAR = variance

Exact calculation of the prediction error variance requires that the full relationship matrix A^{-1} be calculated. Unless the full relationship matrix is constructed directly, the prediction error variance must be estimated from the effective progeny number (EPN). The diagonal elements of the $|Z'MZ + A^{-1}|$ matrix (see equation 5) furnish the EPN for each sire (Berger, 1983). The prediction error variance is then approximated by the error variance divided by the EPN (Ufford et al., 1979). Actual progeny number will generally be larger than EPN. Since the progeny data are regressed back towards the mean, the impact of each record and therefore the EPN, are also regressed towards smaller values. Information from related sires does, however, increase the EPN for a sire's EPD. Accuracy values for a single trait of a sire vary from zero to one, with higher values being the most accurate. Zero ACC values are never seen, since this would mean that no records exist on the sire, his progeny or any of his known relatives. Breeders can use the ACC value to consider the reliability of an EPD and the extent to which a sire's EPD can change (plus or minus) in the next published NSE (BIF, 1986).

Contemporary group by sire interactions can be a source of bias if progeny of some sires receive preferential treatment in particular herds. Adjustments to the matrix equations can be made to discount progeny records made in only a few CG (Henderson, 1974). The impact of a single CG will be greatly reduced if the following substitutions are made in the MMS matrices:

- 1) Replace n_{ij} with $(n_{ij}\beta)/(n_{ij} + \beta)$.

2) Replace y_{ij} with $(y_{ij} \beta)/(y_{ij} + \beta)$.

These alterations limit the impact of any one CG to a sire's EPD to β . The value of β is usually equal to the ratio of residual variance to sire by CG covariance.

The models and methods used to compute NSE vary among breed organizations. Usually computing facilities and computational expertise are the limiting factors. Breeds with smaller data sets (i.e., number of registrations) have a distinct advantage and can more easily use multiple trait RAM. Since the research described in this thesis utilized Polled Hereford sires and APHA sire summary EPD values, the NSE methods used by the APHA will be described.

Seven different traits were evaluated in the 1986 APHA NSE: BWT, WWT, YWT, MAT, Carcass Cutability, Marbling Score and Lean Yield of meat. Maternal EPD's are based on the WWT of a sire's daughters' first calf. Including only information from a daughter's first lactation should eliminate some of the selection bias that occurs in later records of the dam.

Contemporary groups are described by herd, sex of calf and weaning date for all APHA calculations (Gibb and Middleton, 1986). Weaning dates are included to consider age of calf and season of year effects on the data. For WWT and YWT EPD the CG's are further divided according to nutritional level. Creep-fed calves are separated from noncreep-fed calves for WWT analysis. Three feeding levels are used to describe YWT CG's; pasture, feedlot, and calves fitted for the showring are separated into different CG's.

The basic sire model with random dam effects is used to calculate BWT, WWT and postweaning gain EPD (Middleton, 1985). The postweaning gain EPD is used to calculate YWT EPD as described earlier. The following is used to generate MMS for sire EPD's.

Equation 10.

$$y = H\rho + Z_2\mu_2 + X\beta + G\gamma + Z_1\mu_1 + \varepsilon$$

where:

H = incidence matrix of fixed herd effects

ρ = vector of fixed herd effects

Z_2 = incidence matrix of random dam effects

μ_2 = vector of random dam effects

X = incidence matrix of fixed CG effects

β = vector of fixed CG effects

Z_1 = incidence matrix of random sire effects

μ_1 = vector of random sire effects

Dam and CG effects are absorbed into the herd effects. The herd effects are then absorbed into the sire equations before sire EPD solutions are calculated. All traits are evaluated independently. Similiar methods are used to solve for MAT EPD, but a simpler model is used by APHA. The MAT EPD model is described below.

Equation 11.

$$y = X\beta + G\gamma + MGS\mu + \epsilon$$

where:

y = vector of WWT's of maternal
grand-progeny

MGS = incidence matrix of random
maternal grand-sire effects

μ = vector of random maternal
grand-sire effects

The appropriate matrix equations, with absorbed effects, were outlined by Quaas and Pollak (1981) and are shown below.

Equation 12.

$$\begin{bmatrix} Q'A^{-1}Q & -QA^{-1}\alpha \\ -A^{-1}Q\alpha & Z'MZ + A^{-1}\alpha \end{bmatrix} \begin{bmatrix} \gamma \\ \mu \end{bmatrix} = \begin{bmatrix} \emptyset \\ Z'My \end{bmatrix}$$

Over 360,000 progeny WWT records were used to calculate WWT EPD values for over 17,000 sires in the 1986 APHA NSE. Of those sires, the 602 sires with the most progeny records were listed in the sire summary. All listed bulls had ACC values of at least .70 for WWT EPD.

RELATED CATTLE BREEDING STUDIES

Current NSE methods assume that environmental effects are strictly random across CG's or can be corrected by use of appropriate correction

factors. Sires must be used in several CG across herds to achieve high EPN and ACC. However no real attempt is made to consider any environmental effects that might dramatically change the EPD's of the sires. Some evidence for genotype by environment interactions in beef cattle does exist in the literature. Genotype by environment interactions may only change the magnitude of EPD differences between sires. A far worse situation occurs if the ranking of sires is altered because of these interactions (Benyshek, 1980).

When lines of indigenous Hereford cattle were selected for growth in Florida and Montana, significant genotype by environment interactions were discovered for BWT, WWT and YWT when germ plasm was exchanged between the two locations (Butts et al., 1971). The locally bred cattle consistently outperformed the introduced genotypes. The design of that experiment maximized the probability of detecting such an interaction since the original selection had occurred in two of the most extreme and divergent climates available in the U.S. Not only were the growth selected lines developed under those conditions, but their ancestors were also locally adapted cattle. Adaptation to the subtropical Florida climate may involve changes in basal metabolic rates (Fields et al., 1969). The continuation of the same study utilized cattle from a common Montana origin (Burns et al., 1979). These cattle were split into two groups and one group was transferred to Florida while the other remained in Montana. Both groups were then selected for growth. Annual exchanges of young sires were used to assess the degree of genotype by environment interaction. Progeny growth (i.e., BWT, WWT and YWT) was significantly

better for both groups when calves were raised in Montana. However progeny of local sires out performed those of introduced sires in Montana and Florida. These genotype by environment interactions were significant after only a few years of selection. The interaction effects were also large enough that sires ranked differently in the two locations. The differences in growth occurred mostly from conception to weaning (Pahnish et al., 1983). Montana appeared to provide a better environment for selection for growth traits in cattle since body weights were higher there for both groups of cattle. However, any improvement in ability to select for growth was not expressed when sires were transferred to Florida.

Three distinct locations in North Carolina (i.e., Tidewater, Piedmont and Upper Mountain locations) were used in a test of postweaning average daily gains (ADG) in steers sired by a common group of Hereford sires (Ahlschwede et al., 1969). Steers were randomly assigned to a corn and soybean feedlot ration or a spring through summer grazing treatment at each location. No significant sire by location or treatment interactions were reported. A similiar study was conducted at the same three North Carolina locations. BWT and WWT, as well as postweaning ADG, were measured for progeny of a common group of Hereford sires (Tess et al., 1984). Some sire by location interactions were demonstrated, but the results showed that sire components varied only in magnitude between locations. After adjusting for differences in sire variance, the genetic correlation for sire BV between locations was greater than .90 for all traits. Thus the sire by location interactions

affected the magnitude of genetic differences among sires, but not the relative rankings of sires.

An Irish study used sires from six dual purpose cattle breeds to inseminate local, privately owned Dairy Shorthorn and Red Friesian cows (Hocking, 1983). Male progeny were fed on pasture or grain diets at the private farms. Hocking compared 300-d weights of grain fed calves to 500-d weights of grass-fed calves and reported a within breed correlation of $.998 \pm .29$ for sire BV between the two feeding regimes. The different ages at evaluation were chosen so that all calves would be at similiar weights.

In a comparison of three Gelbvieh and 17 Fleckvieh sires with progeny at a Texas and a German location, some significant breed by location effects were reported (Aken et al., 1976). The relative rankings of the two breeds did not change between locations; only the magnitude of the weight differences at 280-, 364- and 420-d changed between locations. No sire by location interactions were significant at those ages for sires within a breed. An Australian group of researchers (Roberts et al., 1982) imported semen from outstanding Hereford sires in New Zealand and United Kingdom. The progeny of those sires were compared to progeny of the top Australian Hereford sires. All bulls had comparable progeny performance, so the authors concluded that sires from the three locations were directly comparable and no genotype by environment interaction could be expected. They did not, however, compare rankings of sire BV's in Australia to those in the sire's country of origin.

Wilson et al. (1972) examined data from a designed progeny test of Hereford and Angus sires used in private herds. Two herds per breed per year were compared and no significant sire by herd effects were demonstrated for BWT, WWT or YWT. More recent studies have used field data sets from individual breed organization NSE to examine similar effects. Field data from the American Simmental Association has been utilized by several researchers. Nunn et al. (1978) divided the U.S. into nine regions based on climate and numbers of registered cattle. Progeny results for BWT and WWT were compared between pairs of regions. Birth weight had a significant sire by region interaction only when comparing the Montana region to the Oklahoma-Texas region. Genetic correlations between regions ranged from .86 to 1.0 for BWT and .73 to .78 for WWT. Since that study used early American Simmental Association records, many of the calves were 1/2 or 3/4 Simmental from herds in upgrading programs. The analysis did not include breed of dam effects, so region effects may have been confounded with the different dam breeds that are used across the U.S.

In a study of Maine-Anjou and Simmental data, Buchanan and Nielsen (1979) reported significant interactions of sire with regions and sires with herds within a region for WWT. A contrast of Simmental half sibs in Montana and Texas resulted in a genetic correlation between the two regions of .32 for WWT. The genetic correlation between herds within either Texas or Montana averaged .47 for the WWT of half sibs. Birth weight genetic correlations were much higher and the authors concluded that there was little evidence of sire by region or sire by herd effects

for the BWT of Simmental sired calves. Their results for the Maine-Anjou field data were quite similar and led them to also conclude that Maine-Anjou sired calves demonstrated sire by location effects on WWT and not on BWT. Three-quarter Simmental calves from full-blood Simmental sires also demonstrated sire by herd effects for WWT when examined by Tess et al. (1979). These interactions were larger than the sire variance estimate so a reranking of sires among locations could be expected for WWT EPD values. Burfening et al. (1982) reported significant sire by location effects for calving ease and BWT of Simmental cattle listed in field records. Genetic correlations were nearly 1.0 across regions, so the interactions changed the magnitude of sire effects and not the rankings of the individual sires that they examined. However, the genetic correlations between herds averaged .50, so some reranking may have occurred between herds. Each sire averaged only about 10 progeny per herd, so this correlation has a large standard error.

Polled Hereford data from the APHA were divided into nine regional data sets by Bertrand et al. (1985). Heritability (h^2) estimates for WWT were calculated using half sibs. The estimates of h^2 were .11 for sires used across regions, .17 for sires used within a region and .28 for sires used within a herd. The authors also reported correlations for WWT EPD values generated within one location and compared to those from other locations. Correlations between regions averaged .64, with a range of .50 to .83. Between herds within a region, the correlations averaged .37 and between CG's within a herd, the correlations averaged .59.

The evidence for a genotype by environment interaction suggests that effects on BWT and YWT are possible but seem to be of little consequence. Weaning weight seems to be more susceptible to these interactions and rankings of sire WWT EPD values could vary between locations.

Crossbreeding should not have significant effects on additive genes, since heterosis is caused by nonadditive gene action (Falconer, 1981). However, gene action only occurs in the context of the entire genome (Dickerson, 1962), so heterosis could potentially affect additive gene expression. Increased fitness due to crossbreeding may effect the expression of additive traits if some sires have better specific combining abilities with available females. If such effects are important, commercial producers would be led to seek sires that perform better in crossbred herds rather than those used by straightbred herds. Fortunately for the purebred cattle industry, the literature offers little evidence of superior crossing abilities of specific sires within a breed. Paternal half sib estimates for h^2 of growth traits did not vary between crossbred and straightbred lines of mice (Vinson et al., 1969). The mice, as with cattle, demonstrated moderate to high levels of additive variation for growth traits.

When comparing sire variance components (i.e., half sib covariance estimates) in straightbred, crossbred (F_1) and backcross *Bos indicus* (Brahman) and *Bos taurus* (Hereford) cattle, Miquel and Cartwright (1963) saw no significant differences between crossbred and straightbred cattle. They concluded that selection in crossbreds would be equally as

effective for growth traits as selection within a breed. The use of *Bos indicus* and *Bos taurus* cattle should have maximized the level of heterosis in the Texas environment of their study. Angus, Hereford, Brahman and all the two way cross dams of these breeds were bred to Angus, Hereford and Brahman sires to produce straightbred and backcross progeny (Koger et al., 1975). Ratios representing percentage deviation from CG means were calculated for BWT, WWT, condition score and 20-mo weight. Correlations between crossbred and straightbred half sibs averaged .96 for all trait ratios. Likewise, the size of the sire variance component estimate was not affected by the level of heterosis. The authors concluded that straightbred and crossbred progeny were of equal worth in determining a sire's BV. Significant differences were reported between the performance of individual breeds and breed combinations, but the effects were strictly additive. Another study used Angus, Hereford, Shorthorn and all their F_1 combinations to examine paternal half sib covariances for BWT, WWT, 550-d weight, slaughter weight and carcass traits (Dunn et al., 1970). No significant differences between straightbred and F_1 progeny were shown for sire variance components or heritability estimates.

Estimates of additive variation for BWT, growth and carcass traits did not significantly vary between straightbred Hereford and Angus cattle examined by Cundiff et al. (1975). Polled Hereford sires were then used in their study to sire calves from Hereford and Angus dams. The genetic variance estimates for the growth and carcass traits of the progeny did not vary between the two genetic groups. Polled Hereford sires were

bred to Angus x Holstein F₁ dams to produce three-way cross calves in a study conducted by Wilson et al. (1976). The F₁ dams had higher milk production than straightbred Polled Hereford dams, so the effects of maternal environment on sire variance component estimates could be measured. The authors measured WWT and YWT on 646 crossbred calves and concluded that calves from higher-milking F₁ dams had similar sire variance and heritability estimates as calves from straightbred Polled Hereford dams. The improvement in maternal environment appeared to have only an additive effect on calf performance.

Limousin field data did show some sire by breed of dam interaction on the WWT EPD of Limousin sires (Benyshek, 1979). The correlation between calculated WWT EPD from Limousin x Hereford F₁ and Limousin x Angus F₁ progeny was .46, but dam breeds were confounded with herd and region effects in these data. Benyshek (1980) also cited unpublished work of Massey and Benyshek that utilized the same Limousin field records to examine sire by breed of dam effects on BWT and YWT. Sire by breed of dam effects were significant when they compared Angus to Hereford herds using Limousin sires. Breed of sire also affected h² estimates of BWT in a controlled crossbreeding experiment (Cundiff et al., 1986). Average heritability estimates were .459 ± .008 for sires within a breed and .793 ± .003 for all sires across all 14 sire breeds when bred to Hereford and Angus dams. The breed effects probably were additive in the latter study and the higher across-breed h² reflects between breed differences in average BWT.

Breeding values for fat-corrected milk were calculated separately for straight and crossbred Aryshire, Friesian and Red and White dairy breeds in a controlled breeding study in Sweden (Dim, 1974). The average correlation between two breeding value estimates were over .90, and Dim concluded that crossbred daughters were as valuable as straightbred daughters for proving a sire. Heterosis in cattle does not seem to alter the expression of traits with at least moderate levels of additive variation.

COMPARISONS OF ACTUAL PERFORMANCE TO SIRE BV ESTIMATES

A few studies have compared actual progeny performance for several dairy and beef production traits to BV estimates. Ruvuna and McDaniel (1983) regressed the performance of F_1 and straightbred Holstein and Brown Swiss daughters on the BV of their sires. They sampled a cross section of 95 Holstein and 70 Brown Swiss sires available in the U.S. The regression of F_1 daughter's performance (milk and milkfat production) on sire predicted differences (PD) was .99 and the correlation coefficient was .26, which is higher then expected given the h^2 of milk production. Their expectation for the correlation of performance to PD was equal to one-half the square root of h^2 . The regression of straightbred progeny performance on sire PD was .99 with a correlaton of .21. Ruvuna and McDaniel concluded that sire PD was as accurately predicted from crossbred as straightbred daughters. The PD values used had been previously derived by the USDA from national field

records. The results show that NSE PD values published by the USDA are excellent predictors of the performance of both straightbred and crossbred daughters.

Expected progeny differences published by the American Hereford Association in their annual NSE report were used by Hough et al. (1985) to select the top 1% of the Hereford sires for YWT EPD. These sires were used to produce straightbred progeny in an experimental herd. The experimental design measured the genetic trend for growth in Hereford cattle by comparing progeny from the selected sires to progeny from a control line that used the same sires for each of the 6 y of the study. By the end of the experiment, the selected line had significantly higher BWT, WWT, YWT and yearling hip heights than the control line. Expectations of the sire's BV were not directly compared to progeny performance, but the positive weight differences showed that EPD values from a NSE do have some impact on selection and genetic trend.

Wilton and McWhir (1985) compared the ADG performance of 411 sires with that of their sons using data from central bull test stations. All data were for Hereford bulls, and the older sires were also listed in the NSE of the American Hereford Association. The h^2 of gain in central test stations was estimated to be .50 from sire-son regressions. Correlations between sire EPD and average performance of his sons were .17 for YWT and -.02 for ADG on test. These values were low, but when only sires with 30 or more progeny in their EPD proof were analyzed, the correlations rose to .23 and .20, respectively. The authors calculated expectations for these correlations by the following formula.

Expected Correlation of Progeny Performance to Sire EPD

$$E [r_{pp,epd}] = \left[\frac{nm}{\{4 + (n - 1)h^2\}\{4 + (m - 1)h^2\}} \right]^{1/2} h^2$$

where:

pp = average performance of sons

epd = sire's EPD

n = number of sons

m = number of progeny in EPD proof

h^2 = heritability of trait

The expected correlations were .39 for YWT and .29 for ADG. Wilton and McWhir concluded that the results were close to expectations but no attempt was made to quantify that conclusion. The lower than expected correlations could be of concern if these results can be repeated or if some source of bias can be postulated. The high h^2 of ADG on test contrasts with the low correlations, suggesting that central test station results are not comparable in their contribution to a sire's EPD records from those of progeny raised on farms.

MATERIALS AND METHODS

DAMS

One hundred four, 5-year-old straightbred Angus cows were first bred for this study in spring 1982 and an additional 53 yearling straightbred Angus heifers entered the study in 1983. The older cows were previously in a crossbreeding study and had been bred to Hereford and Hereford x Simmental F₁ sires. In that study, cows calved in either fall or spring. All cows were randomly bred by AI using semen from selected Polled Hereford sires. Cows were culled only for physical problems that would prohibit them from continuing to reproduce or raise a calf to weaning. Four calf crops (1983 through 1986) were produced. The average calving date was within the second week of March in each year and all the cows calved within an 80-d period. The number of calves born in each year for the two age groups of dams are shown in table 1.

Cows grazed pastures that were predominately fescue and received winter supplementation of fescue hay, corn silage and broiler litter. All animals were kept at the Shenandoah Valley Research Station at Steeles Tavern, Virginia. The calves were weaned each year in the third week of October, at an average age of 221 d.

Table 1. Number of Progeny per Dam Group

<u>Age Group</u>	No. of <u>Dams</u>	<u>1983</u>	<u>1984</u>	<u>1985</u>	<u>1986</u>
Old Dams	104	43*	80	65	73
Young Dams	53		43	34	40

*Fall calving cows did not calve in 1983.

Sires

Sires were chosen annually from those listed in the APHA sire summary. Most sires had a minimum ACC of .85 for YWT and MAT EPD's and were chosen to fit into one of the following sire groups: 1) High YWT and high MAT EPD; 2) High YWT and low MAT EPD; 3) Low YWT and high MAT EPD; and 4) Low YWT and low MAT EPD. Some sires with ACC values of less than .85 were used so that the number of sires sampled could be increased. Since only high ACC sires were used, EPD values changed little in subsequent sire summaries. The EPD values listed in table 2 are from the 1986 sire summary. Average BWT, WWT, YWT and MAT EPD's for sires listed in that sire summary were .5, 9.4, 15.1 and 5.2 kg, respectively (Gibb and Middleton, 1986). The four groups of sires were chosen to facilitate the sampling of different genetic types available in the breed and to increase the genetic differences among progeny groups. Table 2 also lists the average EPD values for each group. The correlations between EPD's across groups are shown in table 3. The correlations between YWT and MAT EPD are lower than for sires in the general population because only sires that fit into the divergent groups were selected.

A new sample of sires was used each year, but some of the previous year's sires were always also used to prevent confounding of annual environmental effects with sire effects. The actual numbers of progeny

Table 2. Sire Expected Progeny Difference (EPD) in kg and Accuracy (ACC)

		<u>Trait</u>									
<u>Sire</u>	<u>Group¹</u>	Birth Weight		Weaning Weight		Yearling Weight		Maternal			
		<u>EPD</u>	<u>ACC</u>	<u>EPD</u>	<u>ACC</u>	<u>EPD</u>	<u>ACC</u>	<u>EPD</u>	<u>ACC</u>		
3	HH	2.0	.99	16.6	.99	29.3	.99	12.4	.99		
6	HH	2.1	.96	13.0	.97	20.6	.96	10.7	.94		
14	HH	1.3	.99	12.9	.99	21.2	.99	8.1	.99		
17	HH	0.7	.99	13.5	.99	19.2	.99	13.0	.99		
19	HH	1.1	.99	13.3	.99	24.8	.99	8.6	.99		
23	HH	1.5	.98	17.0	.99	25.1	.98	7.9	.97		
24	HH	1.5	.96	12.9	.97	20.6	.97	12.3	.92		
25	HH	0.0	.99	15.3	.99	25.7	.98	8.3	.95		
37	<u>HH</u>	<u>1.7</u>	<u>.91</u>	<u>9.0</u>	<u>.91</u>	<u>17.2</u>	<u>.87</u>	<u>11.4</u>	<u>.81</u>		
HH	Group	Avg1.3	.97	13.7	.98	22.6	.97	10.3	.95		
2	HL	0.6	.94	10.0	.95	17.2	.94	1.7	.92		
4	HL	0.6	.94	15.1	.94	20.7	.94	3.6	.86		
12	HL	0.2	.98	16.7	.98	25.1	.98	3.4	.96		
13	HL	0.8	.98	13.3	.98	25.4	.98	1.7	.96		
15	HL	2.8	.96	13.6	.97	25.3	.96	5.3	.94		
21	HL	0.5	.94	0.3	.97	4.5	.97	9.0	.91		
26	HL	4.3	.97	16.7	.97	21.5	.97	1.0	.93		
27	HL	4.8	.91	22.1	.91	37.3	.93	-4.2	.74		
28	HL	1.1	.98	12.4	.98	25.4	.97	-2.8	.93		
29	HL	1.5	.97	12.2	.98	21.3	.97	3.1	.94		
38	HL	5.2	.92	22.8	.92	33.8	.87	1.7	.69		
39	HL	2.9	.97	17.1	.97	29.8	.96	-0.1	.91		
40	<u>HL</u>	<u>0.5</u>	<u>.98</u>	<u>10.5</u>	<u>.98</u>	<u>17.4</u>	<u>.98</u>	<u>-1.3</u>	<u>.95</u>		
HL	Group	Avg2.0	.96	14.1	.96	23.4	.96	1.7	.90		
7	LH	-0.9	.86	1.3	.95	3.4	.96	13.6	.87		
8	LH	1.3	.99	7.2	.99	10.3	.99	9.3	.99		
9	LH	-0.5	.79	3.0	.92	9.0	.91	6.5	.83		
10	LH	0.1	.90	0.9	.97	0.7	.98	8.9	.92		
18	LH	-0.5	.94	13.9	.94	17.9	.91	11.1	.77		
30	LH	0.2	.97	4.8	.93	5.7	.91	6.0	.82		
31	LH	0.3	.87	2.1	.97	8.5	.93	7.5	.91		
32	LH	0.2	.86	3.8	.91	2.0	.88	6.6	.84		
41	LH	0.2	.92	2.1	.91	0.7	.89	8.3	.72		
42	<u>LH</u>	<u>-1.2</u>	<u>.87</u>	<u>-0.1</u>	<u>.91</u>	<u>0.0</u>	<u>.87</u>	<u>12.0</u>	<u>.86</u>		
LH	Group	Avg-0.1	.90	3.9	.94	5.8	.92	9.0	.85		

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1	LL	2.0	.98	7.0	.98	9.4	.98	-6.9	.97
5	LL	-0.6	.94	4.3	.96	8.9	.96	-3.3	.93
11	LL	-0.4	.95	6.6	.97	7.0	.97	1.3	.96
16	LL	0.0	.99	2.0	.99	5.2	.99	-3.2	.99
20	LL	0.2	.94	-2.9	.95	-1.5	.94	1.9	.77
22	LL	0.9	.89	1.5	.93	4.6	.93	-4.7	.86
33	LL	1.5	.92	6.2	.94	5.5	.94	-3.8	.83
34	LL	0.2	.89	5.5	.91	8.6	.91	-1.5	.80
35	LL	-0.7	.86	3.8	.95	9.1	.95	-3.0	.88
36	LL	0.5	.94	7.6	.95	11.0	.96	1.6	.89
43	LL	<u>0.0</u>	<u>.93</u>	<u>4.7</u>	<u>.96</u>	<u>8.4</u>	<u>.95</u>	<u>1.4</u>	<u>.90</u>
LL Group Avg.		0.3	.93	4.2	.95	6.9	.95	-1.8	.89

¹Sire groups: HH, high yearling and high maternal EPD's;
HL, high yearling and low maternal EPD's;
LH, low yearling and high maternal EPD's;
LL, low yearling and low maternal EPD's.

Table 3. Correlations between EPD's* of Sires

	Maternal Weight	Yearling Weight	Weaning Weight
Birth Weight	-.23	.69	.71
Weaning Weight	-.03	.96	
Yearling Weight	-.05		

*American Polled Hereford Assn. Expected Progeny Differences.

per sire and per genetic group are shown in table 4. Progeny numbers per sire varied somewhat due to differences in availability of semen.

CALVES

Male calves were castrated shortly after birth. All calves were weighed at birth, weaning and at approximately 1 year of age. After 1983, calf weights at the end of the breeding season and hip heights at weaning were also measured. End of breeding season weights were taken in the first week of August. These last two measurements are not standard production traits used in the industry, but were added to better identify any differences in calf growth patterns. All measurements, except for BWT, were taken on one date each year, so age differences between calves are included in the basic measures. To attempt to eliminate some of the age-of-calf effects, the weights were adjusted to a constant age by calculating an ADG from birth until weighing and adding birth weight to the product of the ADG value and a standard age in days. This method is recommended by BIF (1986) for WWT and YWT calculations. Adjusted 135-d (ADJ135), 205-d (ADJ205) and 365-d (ADJ365) weights were calculated to reflect end of breeding season weight, WWT and YWT, respectively. No selection occurred at weaning and all calves within a sex were handled similarly so there was no need to calculate ADJ365 as the sum of ADJ205 and 160 d postweaning gains. Instead, ADG from birth to 1 year of age was used calculate ADJ365. Weaning hip heights have

Table 4. Progeny per Sire

<u>Sire</u>	<u>Group*</u>	Number of Progeny in:			
		<u>1983</u>	<u>1984</u>	<u>1985</u>	<u>1986</u>
3	HH	7	7		
6	HH	5			
14	HH		8		
17	HH		9	6	
19	HH		5		
23	HH			8	11
24	HH			7	
25	HH			5	7
<u>37</u>	<u>HH</u>				<u>9</u>
Total HH	Group	12	29	26	27
2	HL	2			
4	HL	7	7		
12	HL		7		
13	HL		9		
15	HL		2		
21	HL		1		
26	HL			4	
27	HL			5	
28	HL			8	
29	HL			5	
38	HL				9
39	HL				8
<u>40</u>	<u>HL</u>				<u>9</u>
Total HL	Group	9	26	22	26
7	LH	7	5		
8	LH	6			
9	LH		2		
10	LH		11	4	
18	LH		12		
30	LH			10	
31	LH			7	
32	LH			6	9
41	LH				8
<u>42</u>	<u>LH</u>				<u>11</u>
Total LH	Group	13	30	27	28
1	LL	5			
5	LL	4	10		
11	LL		3		

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16	LL	6		
20	LL	18		
22	LL	1		
33	LL		6	
34	LL		4	9
35	LL		8	
36	LL		6	13
<u>43</u>	<u>LL</u>			<u>10</u>
Total LL Group	9	38	24	34

*See table 2.

also been adjusted for age. Data from the 3 yr in which weaning heights were measured was used to fit the following regression equation.

Equation 14.

$$y_{ijk} = \beta_0 + DAG_i + YR_j + DAGxYR + SX_k + \beta_1 WAGE$$

where:

y_{ijk} = weaning hip height of progeny

β_0 = intercept

DAG_i = fixed effect of i^{th} dam age group

YR_j = fixed effect of j^{th} year

SX_k = fixed of k^{th} sex

β_1 = regression coefficient of hip height
on age at weaning

WAGE = calf age at weaning (d)

Estimated values for β_0 and β_1 were 76 cm and .11 cm/d, respectively. Adjusted weaning hip heights (ADJWHT) of calves were adjusted to constant age of 205 d by calculating average daily increase in hip height beyond 76 cm and multiplying that value by 205-d.

Calves were used in several nutritional and grazing studies concurrent to this genetics study. Some of the treatment effects were large enough to bias estimates of genetic effects, so additive adjustments were made to eliminate known treatment differences. General linear models were used to test the significance of treatments. Every treatment was tested within a year and sex of calf group, so no other effects were needed in the model. The actual adjustments that were used are listed

below under Preliminary Results. After weaning, the heifers were grazed on pasture while the steer calves entered a feedlot for nutritional studies.

Table 5 lists the annual number of progeny evaluated for each trait. Loss of calves from birth to weaning represents actual death losses. The reduction in calf numbers after weaning is primarily due to the removal of some steer calves from the project. Some of these steers were used in projects that resulted in values for ADJ365 that could not be accurately compared to data from the other steers, even with additive adjustments. Generally these studies used small groups of steers and it was difficult to estimate treatment effects and make reasonable additive adjustments.

PRELIMINARY RESULTS

In 1983 and 1984 all steer calves were randomly assigned at birth to one of three growth-promotant treatment groups. At an average age of about 4 mo, one group received zeranol implants, another received estradiol-17 β implants and the third group received no treatment and was used as a control. The least squares estimates for treatment effect in each of the 2 yr of the study were pooled to make the following additive adjustments so that all calves would be comparable to the control group: -10.0 kg from WWT of zeranol treated calves and -.5 kg from WWT of estradiol-17 β treated calves. Adjusted weaning hip heights and ADJ365

Table 5. Number of Progeny Evaluated

<u>Trait</u>	<u>1983</u>	<u>1984</u>	<u>1985</u>	<u>1986</u>	<u>Total</u>
BWT	43	123	99	113	378
ADJ135		119	85	109	313
ADJ205	43	119	99	109	370
ADJWHT		119	99	109	327
ADJ365	40	108	95	70	313

were not significantly effected by treatments. The ADJ135 weights were also not affected since these weights were taken when the calves were implanted.

Most of the steer calves born in 1983 entered a feedlot trial after weaning. They were divided into four groups, each of which received a ration containing one of the following nitrogen sources: ammonia treated straw, straw treated with ammonia and sulfur, urea or poultry litter. The ration containing ammonia with sulfur caused significantly lower ADG from weaning to 365 d of age, so 17.7 kg was added to the YWT of calves that received this ration.

Two feedlot rations, one with turkey litter and the other with broiler litter, were fed to steers after weaning in 1984. Significant differences in ADG from weaning to 365 d occurred between the two groups. Thus the YWT of calves fed turkey litter was increased by 21.4 kg and the YWT of the calves fed broiler litter was decreased by 21.4 kg. These adjustments made the two groups comparable in overall performance.

Some steer calves in 1985 and 1986 were allowed to creep graze different pastures. This occurred between the dates on which the end of breeding season and weaning weights were taken. The balance of the calves received no special treatment. The creep-grazed calves grazed either fescue pasture treated with the plant growth regulator mefluidide or pasture containing a mixture of fescue and clover. The results of the trial differed between 1985 and 1986, perhaps because of drought conditions in 1986. No significant treatment effects on ADJ205 and ADJWHT were observed in 1985; therefore no adjustments were made. In 1986

the creep grazing treatments had significant effects on ADJ205 only. The ADJ205 of calves grazing fescue-clover and mefluidide-treated fescue pastures were decreased by 27.3 and 22.7 kg, respectively, to make their weights comparable to those of steer calves not used in the study.

Two experimental rations and a control diet were fed to steer calves in 1985. The different rations significantly affected ADJ365. Calves fed ammonia treated straw gained 19.5 kg less than the control group and those fed urea gained 3.6 kg less than the control group. Additive adjustments were made so that calves would be comparable to the control group. In 1986 the different rations that were fed to the steer calves did not have significant effects on ADJ365.

STATISTICAL ANALYSIS

Maternal effects on preweaning growth are generally larger than sire effects. Most probable producing ability (MPPA) for progeny ADJ205 was calculated for each dam to allow for more accurate estimation of sire effects. Calves of the same sex, born in the same year, and from the same sire were considered contemporaries. All ADJ205 records were expressed as deviations from CG means. The production records included records from this study and from the previous study conducted with the older dams. About half of the records on the older dams were from the previous study. The following mixed model was used to calculate MPPA's:

Equation 15.

$$y = DAG\beta_1 + S\beta_2 + Z_1\mu_1$$

where:

y = vector of weaning weight deviations from CG means

DAG = incidence matrix of dam age group
fixed effects (i.e., old and young
dam groups)

β_1 = vector of dam age group fixed
effects

S = incidence matrix of calving season
fixed effects (i.e., fall and spring)

β_2 = vector of calving season fixed
effects

Z_1 = incidence matrix of random dam
effects

μ_1 = vector of random dam effects

The dam incidence matrix was augmented by adding to the diagonal the ratio of error to dam variances. Variance estimates were calculated with all the ADJ205 data and a model that included dam, sire, year, season, dam age group and sex of calf effects. The general linear models procedure of the Statistical Analysis System (SAS, 1982) was used to estimate variance components from maternal half-sib covariance as outlined by Dickerson (1969). The repeatability of the dam effect was estimated to be .40. The resulting mixed model equations also were solved used SAS software. The SAS matrix procedure uses an iterative algorithm to solve systems of linear equations with Gaussian elimination (Forsythe and Moler, 1967).

Progeny BWT's were regressed on sire BWT EPD's using the following model:

Equation 16.

$$y_{ijkl} = \mu + DAG_i + YR_j + DAGxYR + SX_k + \beta_{BWTEPD} + \epsilon_{ijkl}$$

where:

y_{ijkl} = progeny birthweight record

DAG_i = effect of i^{th} dam age group

YR_j = effect of j^{th} year

SX_k = effect of k^{th} calf sex

BWTEPD = American Polled Hereford Assn.
birth weight expected progeny
difference

Regressions of ADJ135, ADJ205, ADJWHT and ADJ365 on WWT EPD were calculated with the following model. The same equation was used to regress progeny performance on YWT EPD and MAT EPD.

Equation 17.

$$y_{ijkl} = \mu + DAG_i + YR_j + DAGxYR + SX_k + \beta_1 MPPA(DAG) + \beta_3 EPD + \epsilon_{ijkl}$$

where:

y_{ijkl} = progeny ADJ135, ADJ205, ADJWHT or ADJ365

MPPA = dam's most probable producing
ability for ADJ205

EPD = APHA estimate of a sire's WWT, YWT
or MAT EPD

The results of the simple regressions can be expressed as correlations between EPD values and progeny performance by multiplying the regression coefficient by the ratio of the standard deviation of EPD's to the standard deviation of progeny performance. Expressing the relationships between EPD values and progeny performance as correlations eliminates scaling differences between EPD's. The value of each EPD estimate as a predictor of progeny performance for all traits can then be easily compared. Two other regression equations were used to further analyze postnatal traits:

Equation 18.

$$y_{ijkl} = \mu + DAG_i + YR_j + DAGxYR + SX_k \\ + \beta_1 MPPA(DAG) + \beta_3 WWTEPD + \beta_4 MATEPD + \varepsilon_{ijkl}$$

where:

WWTEPD = APHA WWT EPD estimate

MATEPD = APHA MAT EPD estimate

Equation 19.

$$y_{ijkl} = \mu + DAG_i + YR_j + DAGxYR + SX_k \\ + \beta_1 MPPA(DAG) + \beta_3 YWTEPD + \beta_4 MATEPD + \varepsilon_{ijkl}$$

where:

YWTEPD = APHA YWT EPD estimate

Equation 19 should indicate any significant differences between the progeny of the different sire groups. Also the relative value of YWT and WWT EPD's as predictors of growth can be compared.

In addition to regressing performance on APHA sire EPD's, new sire EPD estimates was calculated for all the traits measured in this study using only the data from this project. The following model was used to estimate MMS for sire EPD's

Equation 20.

$$y_{ijkl} = \mu + DSY_i + SX_j + D_k + S_l + \epsilon_{ijkl}$$

where:

y_{ijkl} = progeny BWT, ADJ135, ADJ205, ADJWHT or ADJ365

DSY_i = fixed effect of i^{th} dam
age group by year effect

D_k = random effect of k^{th} dam

S_l = random effect of l^{th} sire

The dam and sire incidence matrices were augmented by adding to the diagonals the ratio of residual to random effects. Restriction of sex effects (SX) to a sum of zero made the mixed model equations nonsingular and solvable. Sire variance estimates came from APHA reported values, since sires were highly selected and too many sires were used in too few years to accurately estimate sire components from this data set. The resulting matrix equations, shown below, are similiar to those used by the APHA (Middleton, 1985).

Equation 21.

$$\begin{bmatrix} DSY'DSY & DSY'SX & DSY'Z_1 & DSY'Z_2 \\ SX'DSY & SX'SX & SX'Z_1 & SX'Z_2 \\ Z'_1DSY & Z'_1SX & (Z'_1Z_1 & Z'_1Z_2)^+ & G^{-1} \\ Z'_2DSY & Z'_2SX & (Z'_2Z_1 & Z'_2Z_2)^+ & \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \mu_1 \\ \mu_2 \end{bmatrix} = \begin{bmatrix} DSY'y \\ \emptyset \\ Z'_1y \\ Z'_2y \end{bmatrix}$$

where:

$$G^{-1} = VAR \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix}^{-1} \sigma_{\varepsilon}^2$$

DSY = incidence matrix of fixed dam age group by year effects

SX = incidence matrix of fixed calf sex effects

Z₁ = incidence matrix of random dam effects

Z₂ = incidence matrix of random sire effects

y = vector of progeny records

β_1 = vector estimate of fixed dam age group by year effects

β_2 = vector estimate of fixed sex effects

μ_1 = vector estimate of random dam effects

μ_2 = vector estimate of random sire effects

No equations were absorbed for this small data set, and no sire birth year effects were included.

The MMS for sire EPD's were then correlated with EPD's reported in the 1986 APHA sire summary. The BWT, ADJ205 and ADJ365 EPD values calculated here should be directly comparable to the BWT, WWT and YWT EPD estimates published by APHA. Correlations between these similiar EPD estimates have expectations equal to the product of the ACC values associated with each estimate. Figure 22 illustrates how the EPD values should both correlate to the true genetic value of a sire for that trait (Van Vleck, 1983).

A Z transformation (Morrison, 1976) was used to test if correlations were significantly different from 0 and from the expected values.

Accuracy values for EPD's calculated here are a function of actual progeny numbers and h^2 since no relationships between sires were included in the mixed model equations. The following equation was used to estimate ACC for each EPD estimate calculated from the progeny in this study.

Equation 22.

$$ACC = \left[\frac{nh^2}{4 + (n - 1)h^2} \right]^{1/2}$$

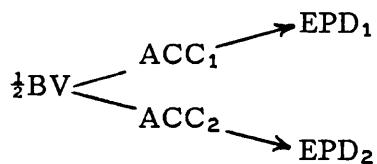
where:

n = number of progeny in EPD proof

h^2 = heritability of trait

This definition of ACC results in expected correlations similiar to those calculated by the method of Wilton and McWhir (1985).

Figure 1. Correlation between independent EPD estimates.



where:

BV = true breeding value of sire

EPD = independent expected progeny difference estimate

ACC = accuracy associated with EPD estimate.

RESULTS AND DISCUSSION

SIRE GROUP PROGENY PERFORMANCE

The average progeny performance for each of the 4 sire groups are shown in table 6. The progeny from high YWT EPD sires were larger at all ages, but the size differences were not always significant. The results also suggest some effect of MAT EPD on progeny growth. Calves in the low MAT groups were smaller than calves from sires with higher MAT EPD's. This trend was consistent for all traits, but was only significant for BWT differences among the low YWT EPD groups. Although differences between progeny groups existed, these differences must be quantified relative to sire EPD differences before making any final conclusions on the value of the APHA EPD estimates.

SOURCES OF VARIATION

An analysis of variation of fixed and random effects was conducted for each trait (tables 7 through 11). Fixed effects defined in equations 16 through 19 and random effects of sires and dams were included in the analysis. For each source of variation the degrees of freedom (df) and mean squares (MS) are listed. Expected mean squares (EMS) are listed for random effects only. There was no significant dam age group (DAG)

Table 6. Average Progeny Performance

<u>Trait</u>	<u>Sire Group*</u>				<u>Avg.</u>
	<u>HH</u>	<u>HL</u>	<u>LH</u>	<u>LL</u>	
BWT, kg	35.9 ^a	35.1 ^{ab}	34.0 ^b	32.5 ^c	34.4
ADJ135, kg	150.7	143.8	146.0	142.5	145.8
ADJ205, kg	192.6 ^a	185.1 ^{ab}	182.7 ^b	179.2 ^b	184.9
ADJWHT, cm	108.1	106.7	105.7	106.0	106.6
ADJ365, kg	289.8 ^a	288.8 ^a	274.6 ^b	274.7 ^b	282.0

*See table 2.

a,b,c: items in the same row with different superscripts are significantly different ($p < .05$) from one another.

effect for any of the traits measured. Year (YR) effects were significant for postnatal weights through weaning. As expected, sex (SX) effects were significant for all traits. These results are consistent with BIF (1986) recommendations that only calves of the same sex and born in the same year be considered as contemporaries. The year effects are a function of both weather and forage growth. Forage availability affects both the milk production of the dam and the direct uptake of forage by the calf. Postweaning growth was less dependent on forage availability, since heifers received supplementation and steers were fed balanced feedlot rations. The nonsignificant year effects on YWT reflects these differences between pre- and postweaning weights.

The older dams in the study were mature and in their peak production years, so no age of dam effects are expected for that group. The younger dams calved first as 2 yr olds and their production levels should have increased over their next three parturitions. Correction factors for age of dam effects on BWT and WWT have been recommended by BIF. Dam age effects are contained in the dam age group by year (DAG x YR) interaction effect listed in the analysis of variance tables. This interaction measures the annual changes in relative performance of the two dam age groups. As the young dams matured their performance improved, while the older dams remained constant or decreased in per-

Table 7. Birthweight Analysis of Variance

<u>Source</u>	<u>df</u>	<u>MS</u>	<u>EMS</u>
DAG	1	6.27	
YR	3	29.31	
SX**	1	111.69	
DAG x YR*	2	51.70	
DAM**	156	26.10	$\sigma^2_e + 2.10\sigma^2_d$
SIRE**	42	32.44	$\sigma^2_e + 4.72\sigma^2_s$
RESIDUAL	172	12.92	σ^2_e

* p<.05; ** p<.01

Table 8. Adjusted 135-d Weight Analysis of Variance

<u>Source</u>	<u>df</u>	<u>MS</u>	<u>EMS</u>
DAG	1	33.9	
YR*	2	3552.0	
SX**	1	2000.2	
DAG x YR	2	152.2	
DAM**	136	368.2	$\sigma^2_e + 1.57\sigma^2_d$
SIRE	38	211.1	$\sigma^2_e + 2.83\sigma^2_s$
RESIDUAL	77	208.0	σ^2_e

* p<.05; ** p<.01

Table 9. Adjusted 205-d Weight Analysis of Variance

<u>Source</u>	<u>df</u>	<u>MS</u>	<u>EMS</u>
DAG	1	656.8	
YR**	3	2535.6	
SX**	1	3448.7	
DAG x YR**	2	1544.4	
DAM**	152	744.0	$\sigma^2_e + 2.11\sigma^2_d$
SIRE	42	347.1	$\sigma^2_e + 4.63\sigma^2_s$
RESIDUAL	168	327.6	σ^2_e

* p<.05; ** p<.01

Table 10. Adjusted 205-d Height Analysis of Variance

<u>Source</u>	<u>df</u>	<u>MS</u>	<u>EMS</u>
DAG	1	1.66	
YR ^{*[*]}	2	359.76	
SX ^{*[*]}	1	94.03	
DAG x YR	2	23.55	
DAM ^{*[*]}	146	23.27	$\sigma^2_e + 1.92\sigma^2_d$
SIRE	38	16.01	$\sigma^2_e + 4.24\sigma^2_s$
RESIDUAL	136	11.49	σ^2_e

* p<.05; ** p<.01

Table 11. Adjusted 365-d Weight Analysis of Variance

<u>Source</u>	<u>df</u>	<u>MS</u>	<u>EMS</u>
DAG	1	1890.4	
YR	3	1975.2	
SX**	1	2975.2	
DAG x YR	2	1055.6	
DAM	145	1520.6	$\sigma^2_e + 1.81\sigma^2_d$
SIRE	42	1311.7	$\sigma^2_e + 3.54\sigma^2_s$
RESIDUAL	118	1271.7	σ^2_e

* p<.05; ** p<.01

formance. The dam age effects did not significantly affect ADJ135, ADJWHT and ADJ365. Dam age should have affected ADJ135 and ADJWHT since these are both measures of early growth that are partially dependent on the milk production of the dam.

Dam effects were large for all preweaning traits. Since a dam contributes to both the genetic and environmental aspects of progeny development, it is reasonable that dam effects would be large. The sire's effect on preweaning growth should be smaller than the dam effects, but still large enough to be apparent. As previously described, the direct interpretation of sire variance components estimated from this data is not recommended because of the design of the breeding program.

A summary of dam and residual variance component estimates are listed in table 12. The APHA h^2 estimates for BWT, WWT and YWT are also listed, since these values were used along with the dam and residual variance estimates to augment the mixed model equations when estimating sire EPD's. Published variance estimates are listed in table 13 for comparison. The values cited by Woldehawariat et al. (1977) are weighted averages from previously published reports. The reported values were weighted by the number of parents and progeny used to determine the estimate. The variance estimates from Wilson et al. (1986) were calculated using American Angus Association and American Hereford Association field records. Generally the APHA h^2 estimates are higher than the estimates derived from the variances listed in table 13.

Table 12. Variance Estimates from Data

<u>Trait</u>	<u>Dam</u>	<u>Residual</u>	<u>APHA h²*</u>
Birth Weight, kg	6.3	12.9	.30
Adj. 135-d Weight, kg	102.0	208.0	
Adj. 205-d Weight, kg	197.4	327.5	.30
Adj. 205-d Height, cm	6.3	12.4	
Adj. 365-d Weight, kg	138.0	1272.0	.40

*American Polled Hereford Assn. heritability estimates (Gibb and Middleton, 1986).

Table 13. Variance Estimates Cited in Literature

<u>Trait</u>	<u>Source</u>	<u>Sire</u>	<u>Dam</u>	<u>Residual</u>
Birth Weight, kg	A	2.52	6.05	13.80
	B	1.00	3.50	8.85
Weaning Weight, kg	A	53.8	269	573
	B	18.9	160	353
Postweaning Gain, kg	B	18.3	45.2	400
Yearling Weight (pasture), kg	A	50.3		468

Source:

A: Woldehawariat et al., 1977.

B: Wilson et al., 1986.

The dam MPPA's estimated for ADJ205 worked well as predictors of dam effects on all post-natal traits (table 14). The linear regression model of calf performance on dam MPPA included all the fixed effects listed in the analysis of variance table 9 (i.e., DAG, YR, SX and DAG x YR). The MMS for dam MPPA resulted in separate MPPA estimates for young and old age group dams. The MPPA values are not comparable across dam age groups, so the regressors listed are for dam MPPA within an age group. The results in table 14 demonstrate the need to account for dam effects when evaluating sires.

REGRESSION OF PROGENY PERFORMANCE ON EPD

The simple regression of progeny performance on APHA EPD estimates resulted in the values listed in table 15. Since EPD is the transmitting ability of the sire, the expectation for the regression of progeny performance on sire EPD is 1 when the same trait is evaluated. Progeny BWT and ADJ365 regressions on BWT and YWT EPD's, respectively, were well within a standard error of their expectations of 1. These two EPD estimates accurately predicted progeny performance.

Weaning weight EPD's should directly predict progeny ADJ205. In this study the APHA WWT EPD had a significant effect on ADJ205 and ADJWHT, but the regressor value for ADJ205 was well below its expected value of 1. Yearling weight EPD was better than WWT EPD as a predictor

Table 14. Linear Regression of Performance on Dam's MPPA¹

<u>Trait</u>	<u>Young Dams</u>	<u>Old Dams</u>
Adj. 135-d Weight, kg	$1.48 \pm .20$	$1.29 \pm .11$
Adj. 205-d Weight, kg	$1.83 \pm .21$	$1.46 \pm .11$
Adj. 205-d Height, cm	$.270 \pm .046$	$.219 \pm .025$
Adj. 365-d Weight, kg	$1.96 \pm .49$	$1.02 \pm .25$

¹Most probable producing ability for Adj. 205-d weight.

Table 15. Linear Regression of Performance on EPD's¹

<u>Trait</u>	<u>EPD</u>	β	<u>r</u>
Birth Weight, kg	Birth Weight	.967 ± .203**	.27
Adj. 135-d Weight, kg	Weaning Weight	.232 ± .141	.08
	Yearling Weight	.153 ± .089	.08
	Maternal	.445 ± .179*	.11
Adj. 205-d Weight, kg	Weaning Weight	.416 ± .139*	.12
	Yearling Weight	.288 ± .086**	.13
	Maternal	.354 ± .163*	.09
Adj. 205-d Height, cm	Weaning Weight	.113 ± .032**	.17
	Yearling Weight	.073 ± .020**	.17
	Maternal	.101 ± .041*	.12
Adj. 365-d Weight, kg	Yearling Weight	.930 ± .191**	.25
	Maternal	.297 ± .373	.04

¹American Polled Hereford Assn. Expected Progeny Difference, kg.

* p<.05; ** p<.01

of ADJ205, as shown by the higher significance level of YWT EPD. Perhaps no genetic differences in early growth rates exist among these Polled Hereford sires in the environment of this study. Yearling weight would be a better indicator of overall size and growth since it has a higher h^2 and is closer to the mature weight of the calf. The insignificant effects of sire WWT and YWT EPD's on ADJ135 also suggest that genetic differences in early growth rates are small.

The significant effect of MAT EPD on ADJ135, ADJ205 and ADJWHT agrees with differences seen in the mean performance of the four sire groups (table 6). It is not clear why only MAT EPD would significantly affect ADJ135. Both the maternal environment and the additive growth genes provided by the dam are included in the APHA MAT EPD, but any additive growth predicted by MAT EPD should be more accurately predicted by WWT EPD. The correlation (r) values listed in table 15 confirm that YWT EPD is as good or better than WWT EPD as a predictor of growth until weaning.

The value of MAT EPD as a predictor of preweaning growth can also be seen in table 16. Partial regressions of progeny performance on both WWT and MAT EPD's reveal that MAT EPD may contribute directly to progeny performance. Maternal EPD values significantly predicted progeny differences in ADJ135 and ADJWHT that were not predicted by WWT EPD. High MAT EPD sires demonstrated an advantage in preweaning growth that cannot be explained by differences in sire WWT EPD's. Some attribute of a sire's EPD for maternal ability may have affected the early growth of calves in this study. The partial regression of progeny per-

formance on YWT and MAT EPD's (table 17) yielded results similiar to those seen for WWT and MAT EPD's. The effects of MAT EPD seen in the partial regression results are consistent with the progeny performance differences among the 4 sire groups (table 6).

Table 16. Partial Regression of Performance on Weaning and Maternal EPD's¹

<u>Trait</u>	<u>Weaning Weight EPD</u>	<u>Maternal EPD</u>
Adj. 135-d Weight, kg	.21± .14	.37± .18*
Adj. 205-d Weight, kg	.35± .14*	.33± .17
Adj. 205-d Height, cm	.019± .006**	.016± .007*
Adj. 365-d Weight, kg	1.34± .31**	.24± .37

¹American Polled Hereford Assn. Expected Progeny Differences.

* p<.05; **p<.01

Table 17. Partial Regression of Performance on Yearling and Maternal EPD's¹

<u>Trait</u>	<u>Yearling Weight EPD</u>	<u>Maternal EPD</u>
Adj. 135-d Weight, kg	.16 ± .09	.44 ± .18*
Adj. 205-d Weight, kg	.28 ± .09**	.31 ± .17
Adj. 205-d Height, cm	.073 ± .020**	.100 ± .040*
Adj. 365-d Weight, kg	.93 ± .19**	.22 ± .36

¹American Polled Hereford Assn. Expected Progeny Differences.

* p<.05; **p<.01

COMPARISON OF EPD ESTIMATES

Sire, dam and error variance components are needed to properly augment the diagonals of the incidence matrices used to calculate MMS for EPD's. In table 12 the APHA estimates of heritability (h^2) are listed. Also listed in that table are the random effect variance estimates used to augment the dam (σ_e^2/σ_d^2) incidence matrix. The ratio of error to sire variance was estimated by $(4/h^2) - 1$. The h^2 estimates used by the APHA were used here for BWT, ADJ205 and ADJ365. No published estimates of the h^2 of ADJWHT and ADJ135 could be found.

No sire EPD estimates were calculated for ADJ135, since no accurate estimates of h^2 could be made for this trait. The sire variance component for ADJ135 estimated from the results in table 8 was very low (1.1 kg^2) and corresponds to a h^2 of less than .02. The regression analysis and the differences in sire group progeny performance (table 6) also suggest very small sire effects on ADJ135. This early measure of calf growth is probably far more indicative of the dam's maternal ability than of differences in growth potential of individual calves. Significant sire effects have been reported for calf weights at 4 mo of age (Brown et al., 1972), but that study fitted growth curves using weights taken at 4 mo intervals. Their conclusions were based on differences in the prediction curves and not on actual weights. Calf weight at 4 mo of age may not have demonstrated large sire effects in their study, if it had been analyzed independently of the later weight measures. An h^2 estimate of .35 was used to calculate sire EPD's for ADJWHT. This appears to be a

reasonable value since it is intermediate between the h^2 estimates for ADJ205 and ADJ365. Hip heights at later ages should have higher h^2 since they are closer to more highly heritable mature body measures (Berg and Butterfield, 1976). The h^2 of hip heights of 15 mo old heifers was estimated to be .54 and .75 in two studies conducted by Neville et al. (1978).

After sire EPD estimates were calculated for BWT, ADJ205, ADJWHT and ADJ365 they were correlated with the EPD estimates listed in the 1986 APHA sire summary. The correlations between the EPD estimates are listed in table 18. The APHA EPD estimates for BWT, WWT and YWT were significantly correlated with progeny performance for BWT, ADJWHT and ADJ365. Closer examination reveals that the APHA YWT EPD had a higher correlation with the EPD estimates for ADJ205 and ADJWHT than did the APHA WWT EPD estimate. This may indicate that only differences in size are measured by the APHA WWT and YWT EPD estimates. Differences in early growth rates of calves were not predicted by the WWT EPD. In such a case the YWT EPD estimate may be a better predictor of WWT since it is closer to the mature weight of the calves and has a higher h^2 .

Only the MAT EPD estimate reported by APHA had a significant correlation with ADJ205 EPD estimated here. The MAT EPD estimate includes both the maternal environmental and the direct genetic components of WWT, so a positive correlation can be expected. The MAT EPD should not, however, be a better predictor of WWT than the WWT EPD of a bull.

Table 18. Correlations between APHA¹ and Data EPD² Estimates.

<u>Data Estimate</u>		APHA Estimate		
	<u>Birth</u>	<u>Weaning</u>	<u>Yearling</u>	<u>Maternal</u>
Birth Weight	.49**	.47**	.48**	.25
Adj. 205-d Weight	.26	.26	.30	.31*
Adj. 205-d Height	.42**	.43**	.45**	.28
Adj. 365-d Weight	.49**	.60**	.66**	.10

¹American Polled Hereford Assn.

²Expected Progeny Difference.

* p<.05; ** p<.01

The WWT EPD is calculated directly from a larger set of half-sib progeny and should be more accurate. These results may reflect actual advantages that high MAT EPD sires have in producing progeny in the environment of this study. The higher correlation of APHA MAT EPD to ADJ205 EPD estimate may reflect the value of the different models used by APHA to estimate WWT and MAT EPD's.

The BWT EPD estimate from this data set is significantly correlated with APHA EPD estimates for BWT, WWT and YWT. This is expected given the positive correlation between BWT and the other growth traits. The reported correlation with MAT EPD is not expected, since the correlation between MAT and BWT EPD's was negative for this group of sires (table 3).

A significant positive correlation among sire EPD estimates does not prohibit the reranking of sires between the two estimates (Robertson, 1959). In a data set of this size, sampling errors can be large. The expectations for genetic correlations between traits which should be genetically similar are listed in table 19. The expectations were calculated as the product of the ACC values associated with the two EPD estimates.

The APHA BWT and YWT EPD correlations with BWT and ADJ365 EPD estimates, respectively, are close to expectations. The WWT EPD had a significantly lower than expected correlation with ADJ205 EPD estimates. This is consistent with the earlier discussion of the poor predictive value of APHA WWT EPD estimates. The actual h^2 of WWT may be lower than the .30 value used by the APHA. The ratio of actual to

Table 19. Comparison of Actual (r) and Expected [$E(r)$] Correlations.

<u>Traits</u>	<u>$E(r)$</u>	<u>r</u>	<u>$r/E(r)$</u>
Birth Weight-Birth	.57	.49	.86
Adj. 205-d Weight-Weaning	.58	.26*	.45
Adj. 365-d Weight-Yearling	.60	.66	1.10

*significant ($p < .05$) deviation from expectation.

expected correlations is an estimate of genetic correlations between the two EPD estimates. A genetic correlation below 1 suggests that the EPD estimates were made on correlated rather than identical traits.

GENERAL DISCUSSION AND CONCLUSIONS

The BWT and YWT of crossbred calves in this study were accurately predicted by APHA BWT and YWT EPD estimates, respectively. The results of APHA NSE should be directly applicable to commercial cattle producers seeking improvement in BWT and YWT traits of crossbred calves.

The APHA WWT EPD estimates were poor predictors of preweaning growth of calves in this study. Previous studies have reported lower than expected h^2 and large genotype by environment interactions for WWT. The h^2 estimate that is used by APHA (.30) is probably too high. A lower h^2 and significant genotype by environment interactions could explain the poor predictive value of WWT EPD estimates. Actual preweaning growth differences among calves were better predicted by YWT than WWT EPD's. The correlation between WWT and YWT is high since WWT is a large component of YWT. Presumably WWT EPD would predict genetic differences among sires for early growth. No evidence from this study suggests that WWT EPD predicts early growth rates of progeny better than YWT EPD. Both EPD's measure growth and are correlated to mature body size. If rate of gain differences are primarily a function of mature size, then YWT EPD's should be a better estimate of growth rates since YWT's are measured closer to the mature end point of cattle. The h^2 of YWT is also higher than that of WWT.

There was however, evidence from this study to suggest that progeny do vary in growth patterns, since the high MAT EPD sires produced larger calves at 135 d and at weaning. Weaning weights are usually measured at about 205 d of age and an earlier weight may be required to detect genetic differences in early growth.

The effects of MAT EPD on preweaning growth were unexpected. It is difficult to postulate why MAT EPD's predicted growth differences that WWT EPD's could not predict. The progeny of high MAT EPD sires may have a biological advantage in the environment of this study. Such an explanation would be difficult to defend. If the high MAT progeny do have an advantage, then some correlation between maternal ability and preweaning growth must exist in the environment of this study. A similiar correlation must not exist in the environments in which the APHA sire proofs were made; otherwise the advantage of high MAT EPD sires would have been reflected in their WWT EPD's.

The mixed models used by APHA to evaluate sires are different for WWT and MAT EPD estimates. The APHA WWT EPD sire model is better designed to account for environmental and assortative mating effects than is their MAT EPD sire model. Effects of herd and both parents are considered in the WWT EPD sire model and not in the MAT EPD sire model. The different sire models used by APHA should favor WWT EPD as the best predictor of preweaning growth. A multiple trait model may be required to accurately partition the effects of maternal ability and additive genes for preweaning growth.

The sires used in this study were selected to create a sire population with no correlation between YWT and MAT EPD's. This population is not representative of the entire population of Polled Hereford sires by design. A positive correlation between APHA YWT and MAT EPD's should exist in the general population due to the method used to calculate MAT EPD. Perhaps the sires used in this study demonstrate no correlation between YWT and MAT EPD because of estimation bias. The sires may have a positive correlation between YWT and MAT and this group of sires is not genetically unique from the general population. The uncorrelated YWT and MAT EPD's of the selected sires may exist only because of estimation errors. These sires all have high ACC and have therefore, been widely used in Polled Hereford herds, so it is hard to rationalize significant prediction errors in their APHA EPD estimates. Some unidentified source of bias could be the cause of a consistent prediction error in APHA NSE calculations for MAT and WWT EPD's.

The large impact of dam effects on progeny growth seen in this study suggest the importance of using sires that will contribute to the quality of dams in the herd. Since the high MAT and YWT EPD sires used in this study produced the largest calves, it appears very advantageous to use high MAT EPD sires in commercial cattle herds. Improvements in calf growth and in maternal ability should occur with the use of high MAT EPD sires.

LITERATURE CITED

- Ahlschwede, W. T., E. V. Dillard, J. E. Legates and O. W. Robison. 1969. Sire-environment interaction effects on steer growth. *J. Anim. Sci.* 28:130 (Abstr.).
- Aken, W. D., G. Averdunk, C. R. Long and T. C. Cartwright. 1976. Genotype, environment and interaction effects on growth characters. *J. Anim. Sci.* 43:212 (Abstr.).
- Anderson, J. H. and R. L. Willham. 1978. Weaning weight correction factors from Angus field data. *J. Anim. Sci.* 47:124.
- Benyshek, L. L. 1979. Sire by breed of dam interaction for weaning weight in Limousin sire evaluation. *J. Anim. Sci.* 49:63.
- Benyshek, L. L. 1980. The effect of genotype by environment interaction on national sire evaluation programs. In: Proc. Beef Improvement Fed. Symp. and Ann. Meet., p.32.
- Benyshek, L. L. 1986. Sire evaluation- Where we've come from. In: Proc. Beef Improvement Fed. Symp. and Ann. Meet., p.58.
- Berg, R. J. and R. M. Butterfield. 1976. New Concepts of Cattle Growth. Sydney University Press, Australia.
- Berger, P. J. 1983. Current sire evaluation. In: Prediction of Genetic Values for Beef Cattle: Proceedings of a Workshop. Winrock International, Morrilton, Arkansas.
- Bertrand, J. K., L. L. Benyshek and D. E. Little. 1985. The reduced animal mixed model equations for national sire evaluation. In: Proc. Beef Improvement Fed. Symp. and Ann. Meet., p.61.
- Bertrand, J. K., P. J. Berger and R. L. Willham. 1985. Sire x environment interactions in beef cattle weaning weight field data. *J. Anim. Sci.* 60:1396.
- BIF. 1986. Beef Improvement Federation Guidelines for Uniform Beef Improvement Programs. 5th Ed. North Carolina University, Raleigh.
- Brown, J. E., C. J. Brown and W. T. Butts. 1972. A discussion of the genetic aspects of weight, mature weight, and rate of maturing in Hereford and Angus cattle. *J. Anim. Sci.* 34:525.
- Buchanan, D. S. and M. K. Nielsen. 1979. Sire by environment interactions in beef cattle field data. *J. Anim. Sci.* 48:307.

- Burfening, P. J., D. D. Kress and R. L. Friedrich. 1982. Sire x region of United States and herd interactions for calving ease and birthweight. *J. Anim. Sci.* 55:765.
- Burns, W. C., M. Koger, W. T. Butts, O. F. Pahnish and R. L. Blackwell. 1979. *J. Anim. Sci.* 49:403.
- Butts, W. T., M. Koger, O. F. Pahnish, W. C. Burns and E. J. Warwick. 1971. *J. Anim. Sci.* 33:923.
- Cundiff, L. V., K. E. Gregory and C. E. Long. 1975. Genetic variation among and within herds of Angus and Hereford cattle. *J. Anim. Sci.* 41:1270.
- Cundiff, L. V., M. D. MacNeil, K. E. Gregory and R. M. Koch. 1986. Between- and within-breed genetic analysis of calving traits and survival to weaning in beef cattle. *J. Anim. Sci.* 63:27.
- Dickerson, G. E. 1962. Applications of genetic-environmental interactions in animal breeding. *Anim. Prod.* 4:47.
- Dickerson, G. E. 1969. Techniques for research in quantitative animal genetics. In: *Techniques and Procedures in Animal Science Research*. American Society of Animal Science. Albany, New York.
- Dim, N. I. 1974. Progeny testing of dairy cattle on purebreds and crossbreds. In: *Proc. 1st World Cong. on Genet. Appl. to Livestock Prod.* Vol. III. p.667.
- Dunn, R. J., W. T. Magee, K. E. Gregory, L. V. Cundiff and R. M. Koch. 1970. Genetic parameters in straightbred and crossbred beef cattle. *J. Anim. Sci.* 31:656.
- Elzo, M. A., E. J. Pollak and R. L. Quaas. 1987. Genetic trends in Simmental population. In: *1987 American Simmental Association Sire Summary*, American Simmental Assoc., Bozeman, Montana.
- Falconer, D. S. 1981. *Introduction to Quantitative Genetics*. 2nd Ed. Longman Group Limited. Essex, England.
- Fields, M. J., W. C. Burns, M. Koger, A. C. Warnick. 1969. Bovine blood thyroid hormone levels at two locations. *J. Anim. Sci.* 29:189 (Abstr.).
- Forsythe, G. E. and C. B. Moler. 1967. *Computer Solution of Linear Algebraic Systems*. Prentice-Hall. Englewood Cliffs, New Jersey.
- Gibb, J. and B. K. Middleton. 1986. Introduction. In: *1986 Polled Hereford Sire Summary*. American Polled Hereford Assoc. Kansas City, Missouri.

- Goddard, M. 1985. A method of comparing sires evaluated in different countries. *Livestock Prod. Sci.* 13:321.
- Henderson, C. R. 1973. Sire evaluation and genetic trends. In: *Proc. Anim. Breed. and Genet. Symp.* in honor of Dr. Jay L. Lush. American Society of Animal Science. Champaign, Illinois.
- Henderson, C. R. 1974. General flexibility of linear model techniques for sire evaluation. *J. Dairy Sci.* 57:963.
- Henderson, C. R. 1975. Rapid method for computing the inverse of a relationship matrix. *J. Dairy Sci.* 32:706.
- Henderson, C. R. and R. L. Quaas. 1976. Multiple trait evaluation using relatives' records. *J. Anim. Sci.* 43:1188.
- Hickman, C. G., A. J. Lee and K. Gravir. 1969. Genotype x season x method interaction in evaluating dairy sires from progeny records. *Can. J. Anim. Sci.* 49:151.
- Hocking, P. M. 1983. Live weights at fixed ages of Dairy Shorthorn, Red Friesian, Red Holstein, Meuse-Rhine-Yssel, Simmental and other sire breed progeny of Dairy Shorthorn, Red Friesian and crossbred dams, and estimates of heterosis and apparent heritability. *Anim. Prod.* 36:285.
- Hough,, J. D., L. L. Benyshek and J. W. Mabry. 1985. Direct and correlated response to yearling weight selection in Hereford cattle using nationally evaluated sires. *J. Anim. Sci.* 61:1335.
- Kennedy, B. W. and C. R. Henderson. 1975. Components of variance of growth traits among Hereford and Aberdeen Angus calves. *Can. J. Anim. Sci.* 55:493.
- Koger, M. A., A. G. Jilek, W. C. Burris and J. R. Crockett. 1975. Sire effects for specific combining ability in purebred and crossbred cattle. *J. Anim. Sci.* 40:230.
- Leighton, E. A., R. L. Willham and P. J. Berger. 1982. Factors influencing weaning weight in Hereford cattle and adjustment factors to correct for these effects. *J. Anim. Sci.* 54:957.
- Lush, J. L. 1935. Progeny test and performance as indicators of an animal's breeding value. *J. Dairy Sci.* 18:1.
- Morrison, D. F. 1976. *Multivariate Statistical Methods*. 2nd Ed. McGraw-Hill, Inc. New York.
- Miquel, C. and T. C. Cartwright. 1963. Comparison of heritabilities in crossbred and purebred cattle. *J. Anim. Sci.* 22:821 (Abstr.).

- Nelson, T. C., R. E. Short, J. J. Urick and W. L. Reynolds. 1984. Genetic variance components of birth weight in a herd of unselected cattle. *J. Anim. Sci.* 59:1459.
- Neville, Jr., W. E., J. B. Smith, B. G. Mullinix, Jr. and W. C. McCormick. 1978. Relationships between pelvic dimensions and hip heights and estimates of heritabilities. *J. Anim. Sci.* 47:1089.
- Nunn, T. R., D. D. Kress, P. J. Burfening and D. Varinum. 1978. Region by sire interaction for reproduction traits in beef cattle. *J. Anim. Sci.* 46:957.
- Pahnish, O. F., M. Koger, J. J. Urick, W. C. Burns, W. T. Butts and G. V. Richardson. 1983. Genotype x environment interaction in Hereford cattle: III. Postweaning traits of heifers. *J. Anim. Sci.* 56:1039.
- Parnell, P. F., R. L. Baker and J. L. Foulley. 1986. The efficiency and place of multi-herd animal evaluation procedures for beef cattle. In: Proc. 3rd World Cong. on Genet. Appl. to Livestock Prod. Vol. IX. p.373.
- Pollak, E. J. and R. L. Quaas. 1983. Genetic evaluation of beef cattle from performance test data. In: Prediction of Genetic Values for Beef Cattle: Proceedings of a Workshop. Winrock Inter., Arkansas.
- Quaas, R. L. and E. J. Pollak. 1980. Mixed model methodology for farm and ranch beef cattle testing programs. *J. Anim. Sci.* 51:1277.
- Quaas, R. L. and E. J. Pollak. 1981. Modified equations for sire models with groups. *J. Dairy Sci.* 64:1868.
- Roberts, E. M., R. F. Scott and J. W. James. 1982. Comparison of breeding values of United Kingdom, New Zealand and Australian Herefords. In: Proc. 2nd World Cong. on Genet. Appl. to Livestock Prod. Vol. I. p.475.
- Robertson, A. 1959. The sampling variance of the genetic correlation coefficient. *Biometrics* 15:469.
- Ruvuna, F. and B. T. McDaniel. 1983. Relationships of predicted differences of dairy bulls and the performance of their crossbred progeny. *J. Anim. Sci.* 57:1133.
- SAS. 1982. SAS User's Guide. Statistical Aanalysis System, Inc. Cary, North Carolina.
- Tess, M. W., K. E. Jeske, E. V. Dillard and O. W. Robison. 1984. Sire x environment interactions for growth traits of Hereford cattle. *J. Anim. Sci.* 59:1467.

- Tess, M. W., D. D. Kress, P. J. Burfening and R. L. Friedrich. 1979. Sire by environment interactions in Simmental-sired calves. *J. Anim. Sci.* 49:964.
- Ufford, G. R., C. R. Henderson and L. D. Van Vleck. 1979. An approxiamate procedure for determining prediction error variances of sire evaluations. *J. Dairy Sci.* 62:621.
- Vinson, W. E., E. J. Eisen and O. W. Robison. 1969. Predicted response to selection for crossbred performance in mice. *J. Anim. Sci.* 28:725.
- Van Vleck, D. 1983. Notes on the Theory and Application of Selection Principles for the Genetic Improvement of Animals. Cornell University. Ithaca, New York.
- Warwick, E. J. 1980. Where have we been? A historic look at sire evaluation. In: Proc. Beef Improvement Fed. Symp. and Ann. Meet., p.24.
- Wilson, D. E., R. L. Willham and P. J. Berger. 1985. Mixed model methodology for unifying within-herd and national beef sire evaluation. *J. Anim. Sci.* 61:814.
- Wilson, D. E., P. J. Berger and R. L. Willham. 1986. Estimates of beef growth trait variances and heritabilities determined from field records. *J. Anim. Sci.* 63:386.
- Wilson, L. L., J. R. McCurley, J. H. Ziegler and J. L. Watkins. 1976. Genetic paramaters of live and carcass characters from progeny of Polled Hereford sires and Angus-Holstein cows. *J. Anim. Sci.* 43:569.
- Wilson, L. L., W. H. Rishel and W. R. Harvey. 1972. Influence of herd, sire and herd x sire on live and carcass characters of beef cattle. *J. Anim. Sci.* 35:502.
- Wilton, J. W. and J. McWhir. 1985. Individual and progeny estimates of growth in station and herd tests. *J. Anim. Sci.* 61:107.
- Woldehawariat, G., M. A. Talamantes, R. R. Petty, Jr. and T. C. Cartwright. 1977. A summary of genetic and environmental statistics for growth and conformation characters of young beef cattle. Texas Agr. Exp. Sta. Tech. Rep. No. 103.
- Wyatt, W. E. and D. E. Franke. 1986. Estimation of direct and maternal additive heterotic effects for preweaning growth traits in cattle breeds represented in the Southern Region. Southern Coop. Series Bull. No. 310.
- Zollinger, W. A. and M. K. Nielsen. 1984. An evaluation of bias in estimated breeding values for weaning weight in Angus beef cattle field

records. II. Estimates of bias due to genetic trend. J. Anim. Sci. 58:550.

Zollinger, W. A. and M. K. Nielsen. 1984. An evaluation of bias in estimated breeding values for weaning weight in Angus beef cattle field records. III. Estimates of bias due to nonrandom mating. J. Anim. Sci. 58:556.

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